

## Appendix 1: Alignment of AAC50763 and SEQ ID NO: 27 of Umezawa et al.

BLASTP 2.2.22+

Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference for compositional score matrix adjustment: Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schaffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

RID: E47D8T1E114

Query= gi|1561728|gb|AAC50763.1| transcription factor RTEF-1 [Homo sapiens]  
Length=434

Sequences producing significant alignments:	Score (Bits)	E Value
1cl 19493 SID_27	874	0.0

## ALIGNMENTS

>1cl|19493 SID\_27  
Length=427

Score = 874 bits (2258), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 419/427 (98%), Positives = 419/427 (98%), Gaps = 0/427 (0%)

Query	8	ITSNEWSSPTSPGEGSTASGGSQLDKPIDNDGEGVWSPDIEQSFQEALAIYPPCGRRKII	67
Sbjct	1	ITSNEWSSPTSPGEGSTASGGSQLDKPIDND EGVWSPDIEQSFQEALAIYPPCGRRKII	60
Query	68	LSDEGKMYGRNELIARYIKLRTGKTRTRKQVSSHQVLARRKAREIQAKLKDQAAKDKAL	127
Sbjct	61	LSDEGKMYGRNELIARYIKLRTGKTRTRKQVSSHQVLARRKAREIQAKLKDQAAKDKAL	120
Query	128	QSMAMSSAQIIISATAFHSSMLARGPGRPAVSGFWQGLPGQAETSHDVKPFSQQTYAV	187
Sbjct	121	QSMAMSSAQIIISATAFHSSMALARGPGRPAVSGFWQGLPGQAGTSHDVKPFSQQTYAV	180
Query	188	QPPLPLPGFESPAGPAPSPSAPPAPPWQGRRRGSSKLWMLFSAFLEQQQDPDTYNKHLF	247
Sbjct	181	QPPLPLPGFESPAGPAPSPSAPPAPPWQGRSVASSKLWMLFSAFLEQQQDPDTYNKHLF	240
Query	248	VHIGQSSPSYLRLPYLEAVDIRQIYDKFPEKKGGGLKDLFERGPSNAFFLVKFWADLNTNIE	307
Sbjct	241	VHIGQSSPSY PYLEAVDIRQIYDKFPEKKGGGLKDLFERGPSNAFFLVKFWADLNTNIE	300
Query	308	DEGSSFYGVSSQYESPENMIITCTKVCSEFGKQVVEKVEYARYENGHYSYRIHRSPLC	367
Sbjct	301	DEGSSFYGVSSQYESPENMIITCTKVCSEFGKQVVEKVEYARYENGHYSYRIHRSPLC	360
Query	368	EYMINFIHKLKHLPEKYMMSVLENFTILQVVTNRDQTETLLCIAYVFEVSASEHAQH	427

Sbjct	361	EYMINFIHKLKHLPEKYMMNSVLENFTILQVVVITNRDTQETLLCIAYVFEVSASEHGAQHH	
		EYMINFIHKLKHLPEKYMMNSVLENFTILQVVVITNRDTQETLLCIAYVFEVSASEHGAQHH	420
Query	428	IYRLVKE	434
		IYRLVKE	
Sbjct	421	IYRLVKE	427